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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=1; day=24; hr=12; min=38; sec=29; ms=765;]

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Application No:	10565183	Version No:	1.1
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No. of SeqIDs Defined:	4
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SEQUENCE LISTING

<110> VERMEIJ, Paul

<120> Hybrid toxins comprising shiga or shiga-like toxin
subunits fused to escherichia coli heat labile
enterotoxin subunits and vaccines thereof

<130> I-2003.006 US

<140> 10565183

<141> 2008-01-16

<150> PCT/EP2004/051522

<151> 2004-07-16

<150> EP 03077266.9

<151> 2003-07-21

<160> 4

<170> PatentIn version 3.3

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<212> DNA

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<221> CDS

<222> (1)..(954)

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Gln Gln Ser Tyr Val Ser Ser Leu Asn Ser Ile Arg Thr Val Ile Ser	
35 40 45	

acc cct ctt gaa cat ata tct cag gga gct aca tcg gta tcc gtt att	192
Thr Pro Leu Glu His Ile Ser Gln Gly Ala Thr Ser Val Ser Val Ile	
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aat cat aca cca cca gga agt tat att tcc gta ggt ata cga ggg ctt	240
Asn His Thr Pro Pro Gly Ser Tyr Ile Ser Val Gly Ile Arg Gly Leu	
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gat gtt tat cag gag cgt ttt gac cat ctt cgt ctg att att gaa cga	288
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85 90 95	

aat aat tta tat gtg gct gga ttt gtt aat acg aca aca aat act ttc	336
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100 105 110	
tac aga ttt tca gat ttt gca cat ata tca ttg ccc ggt gtg aca act	384
Tyr Arg Phe Ser Asp Phe Ala His Ile Ser Leu Pro Gly Val Thr Thr	
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att tcc atg aca acg gac agc agt tat acc act ctg caa cgt gtc gca	432
Ile Ser Met Thr Thr Asp Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala	
130 135 140	
gcg ctg gaa cgt tcc gga atg caa atc agt cgt cac tca ctg gtt tca	480
Ala Leu Glu Arg Ser Gly Met Gln Ile Ser Arg His Ser Leu Val Ser	
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Ser Tyr Leu Ala Leu Met Glu Phe Ser Gly Asn Thr Met Thr Arg Asp	
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Ala Ser Arg Ala Val Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu	
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cgg ttc agg caa ata cag aga gaa ttt cgt ctg gca ctg tct gaa act	624
Arg Phe Arg Gln Ile Gln Arg Glu Phe Arg Leu Ala Leu Ser Glu Thr	
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Ala Pro Val Tyr Thr Met Thr Pro Glu Asp Val Asp Leu Thr Leu Asn	
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225 230 235 240	
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Val Arg Val Gly Arg Ile Ser Phe Asn Asn Ile Ser Ala Ile Leu Gly	
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Gly Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu	
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Arg Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser Asp Tyr Gln	
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Ser Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu	
305 310 315	

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Gln Gln Ser Tyr Val Ser Ser Leu Asn Ser Ile Arg Thr Val Ile Ser
35 40 45

Thr Pro Leu Glu His Ile Ser Gln Gly Ala Thr Ser Val Ser Val Ile
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Asn His Thr Pro Pro Gly Ser Tyr Ile Ser Val Gly Ile Arg Gly Leu
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Asp Val Tyr Gln Glu Arg Phe Asp His Leu Arg Leu Ile Ile Glu Arg
85 90 95

Asn Asn Leu Tyr Val Ala Gly Phe Val Asn Thr Thr Thr Asn Thr Phe
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Tyr Arg Phe Ser Asp Phe Ala His Ile Ser Leu Pro Gly Val Thr Thr
115 120 125

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130 135 140

Ala Leu Glu Arg Ser Gly Met Gln Ile Ser Arg His Ser Leu Val Ser
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Ser Tyr Leu Ala Leu Met Glu Phe Ser Gly Asn Thr Met Thr Arg Asp
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180 185 190

Arg Phe Arg Gln Ile Gln Arg Glu Phe Arg Leu Ala Leu Ser Glu Thr
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Trp Gly Arg Ile Ser Asn Val Leu Pro Glu Tyr Arg Gly Glu Ala Gly
225 230 235 240

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Thr Val Ala Val Ile Leu Asn Cys Gly Asn Ser Ser Arg Thr Ile Thr
260 265 270

Gly Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu
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caacgtgtcg cagcgctgga acgttccgga atgcaaata gtcgtcactc actgggtttca	480
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tcagactatc agtcagaggt tgacatatat aacagaattc gggatgaatt atg aat	956
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Lys Val Lys Cys Tyr Val Leu Phe Thr Ala Leu Leu Ser Ser Leu Tyr	
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gca cac gga gct ccc cag act att aca gaa cta tgt tcg gaa tat cgc	1052
Ala His Gly Ala Pro Gln Thr Ile Thr Glu Leu Cys Ser Glu Tyr Arg	
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Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys Ile Leu Ser Tyr Thr Glu	
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tcg atg gca ggc aaa aga gaa atg gtt atc att aca ttt aag agc ggc	1148
Ser Met Ala Gly Lys Arg Glu Met Val Ile Ile Thr Phe Lys Ser Gly	
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gaa aca ttt cag gtc gaa gtc ccg ggc agt caa cat ata gac tcc cag	1196
Glu Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp Ser Gln	
70 75 80	
aaa aaa gcc att gaa agg atg aag gac aca tta aga atc aca tat ctg	1244
Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Thr Tyr Leu	
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100105110

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Ser Gly Glu Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp

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Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Thr

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Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val Trp Asn Asn Lys

100105110

Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Lys Asn

115120